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Molecular genetics of human prion diseases

JOHN COLLINGE AND MARK S. PALMER

Department of Biochemistry and Molecular Genetics, St Mary's Hospital Medical School, Imperial College, London W2 1PG, U.K.

SUMMARY

Human prion diseases occur in inherited, sporadic and acquired forms. The inherited forms are associated with coding mutations in the prion protein gene and the identification of one of these pathogenic mutations allows definitive diagnosis and has resulted in a widening of the previously recognized phenotypic spectrum of these diseases. Study of acquired prion disease provides evidence for genetic susceptibility to development of disease following treatment with contaminated pituitary hormones. Sporadic prion disease occurs predominately in individuals homozygous with respect to a common PrP polymorphism at residue 129. The identification of pathogenic PrP alleles and the role of the codon 129 PrP gene polymorphism in determining susceptibility to prion disease provides strong support for the idea that an abnormal isoform of PrP, PrPSc, is the principal constituent of the prion and that its propagation involves direct PrP-PrP interactions which occur most readily between identical PrP molecules.

1. INTRODUCTION

The prion diseases are a closely related group of neurodegenerative conditions which affect both humans and animals. They have previously been described as the sub-acute spongiform encephalopathies, slow virus diseases and transmissible dementias. The prototypic disease is scrapie, a naturally occurring disease affecting sheep and goats, which has been recognized in the U.K. for over 200 years (McGowan 1922). More recently recognized animal diseases include transmissible mink encephalopathy (Marsh et al. 1991), chronic wasting disease of mule deer and elk (Williams et al. 1980) and bovine spongiform encephalopathy (BSE) (Wells et al. 1987). The recently described feline spongiform encephalopathy of domestic cats (Wyatt et al. 1991) and spongiform encephalopathies of a number of zoo animals (Jeffrey et al. 1988; Kirkwood et al. 1990) are also now recognized as animal prion diseases. It is now clear that the epidemic of BSE among British cattle has resulted from the inclusion of dietary supplements prepared from the rendered carcasses of scrapie-infected sheep and, later, BSE-infected cows (Wilesmith et al. 1988). It seems likely that spongiform encephalopathies of other captive animals have also arisen from such dietary exposure to the transmissible agent. However, the mechanism of transmission of 'natural' sheep scrapie still remains unclear.

Traditionally, the human diseases have been subdivided into kuru, Creutzfeldt–Jakob disease and Gerstmann-Sträussler syndrome, and are all, like the animal diseases, transmissible to a range of experimental animals by intracerebral or other routes of inoculation (Gibbs et al. 1973). Kuru reached epidemic proportions amongst the Fore peoples of Papua New Guinea and was thought to be transmitted by ritualistic cannibalism (Alpers 1987). Other documented examples of case-to-case spread in humans has resulted from a number of iatrogenic routes. These include the use of inadequately sterilized intracerebral electrodes, dura mater and corneal grafting, and most recently treatment with human cadaveric derived pituitary growth hormone and gonadotrophin. Considerable concern has been raised that the inclusion of BSE-infected meat and more specifically offal in the production of human foodstuffs may result in the transmission of BSE to humans, although there is no evidence for this at present.

The spongiform encephalopathies both of animals and humans share common histopathological features. These include the classic triad of spongy degeneration (affecting any part of the cerebral grey matter), neuronal loss and the proliferation and hypertrophy of astrocytes (Beck & Daniel 1987). These changes are accompanied by accumulation in the brain of an abnormal, partially protease-resistant isoform of a host-encoded protein, prion protein, as amyloid (Prusiner 1987). A wide body of experimental evidence suggests that this abnormal, partly protease-resistant isoform of PrP is an essential, and may be the sole, constituent of the transmissible agent. Purified PrP fractions retain infectivity which is resistant to treatment with agents known to inactivate nucleic acids (Prusiner 1987).

The term 'Creutzfeldt-Jakob disease' (CJD) was first used by Spielmeyer in 1922, bringing together the original case report by Creutzfeldt in 1920 with subsequent cases described by Jakob. The term was used in subsequent years to cover a wide range of neurodegenerative conditions, and was not a very clearly defined diagnostic entity. In the late 1950s

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Hadlow (Hadlow 1959) and also Klatzo and colleagues (Klatzo et al. 1959) pointed out the neuropathological similarity between scrapie, kuru and cpp. The successful transmission of kuru in 1966 and cjp in 1968 to the chimpanzee by Gadjusek and colleagues (Gajdusek et al. 1966; Gibbs et al. 1968) led to the emergence of the concept of the transmissible dementias. Experimental transmission work allowed diagnostic criteria for CJD to be reassessed and refined. CJD is currently recognized clinically by the occurrence of a rapidly progressive dementia with myoclonus which may be accompanied by pyramidal signs, cerebellar ataxia or extrapyramidal features. The clinical course is usually rapid and many cases die within three months of onset. The duration of illness in the vast majority of cases is less than 12 months. Routine investigations are generally unhelpful; in particular there is no evidence of an infective process occurring. The only useful investigation is the electroencephalogram which may show characteristic pseudoperiodic sharp wave activity (Cathala & Baron 1987). Neuroimaging reveals only varying degrees of cerebral atrophy. Around 10% of cjp cases present atypically with a longer duration of illness (Brown et al. 1984). The incidence of CID seems remarkably uniform throughout the world where systematic epidemiological surveys have been performed. The incidence is around 0.5 to 1 case per million population per annum, and has an apparently random distribution related only to the local population density (Brown et al. 1987). There are however exceptions to this in the form of three ethnogeographic clusters of CID (see later). Despite its transmissibility, cjp therefore does not epidemiologically resemble an infectious disease. There is no evidence of case to case spread with the exception of the rare iatrogenic cases discussed previously. In addition there is no relationship of the incidence of cjp with local scrapie prevalence. However around 15% of cases of CID occur in a familial

Gerstmann-Sträussler syndrome (GSS) was first described in 1928 by Gerstmann in a single patient (Gerstmann 1928). A more detailed report of this individual and seven other members from the same Austrian family followed in 1936 by Gerstmann, Sträussler and Scheinker (Gerstmann et al. 1936). The condition is also referred to as Gerstmann-Sträussler-Scheinker disease. The classic description of GSS is of a chronic cerebellar ataxia with dementia occurring later in a much more prolonged clinical course. The mean duration of illness is around 5 years. The pathological hallmark of GSS is the presence of multicentric amyloid plaques distributed throughout the brain. Neuronal loss, spongiform change and white matter loss is seen in most cases (Masters et al. 1981). GSS was transmitted to experimental animals in 1981 (Masters et al. 1981). GSS usually occurs in a familial context and like familial cjp the disease segregation suggests an autosomal dominant pattern of inheri-

Partial amino acid sequencing of the N-terminal of PrP isolated from the brains of affected hamsters and subsequent screening of cDNA libraries led to the realisation that the prion protein was encoded by a host chromosomal gene and not, as had previously been thought, by a viral genome (Chesebro et al. 1985; Oesch et al. 1985; Basler et al. 1986). The PrP gene in humans maps to the short arm of chromosome 20 (Sparkes et al. 1986; Robakis et al. 1986). Because all the spongiform encephalopathies are associated with accumulation in the brain of an abnormal isoform of PrP, the PrP gene was clearly a strong candidate gene for genetic linkage studies in GSS and familial forms of сјр. Hsiao et al. in 1989 first reported genetic linkage between the PrP gene and GSS in two families, demonstrating gss to be an autosomal dominant inherited condition in addition to being transmissible to experimental animals by inoculation with brain homogenate (Hsiao et al. 1989). The polymorphism identified by Hsiao and colleagues was not an anonymous DNA marker but a missense mutation at codon 102 of the PrP gene open reading frame which results in a proline to leucine substitution in the mutant protein. Proline 102 is very highly conserved; all mammalian PrP genes sequenced to date encode proline at the corresponding codon. This mutation has now been confirmed in a large number of GSS kindreds in the U.K., U.S.A., Germany, Italy and Japan (Doh ura et al. 1989; Goldgaber et al. 1989; Speer et al. 1991; Kretzschmar et al. 1992) and indeed in the original Austrian family reported by Gerstmann (Kretzschmar et al. 1991). This mutation has not however been seen in several hundred controls. It therefore seemed highly likely on statistical grounds that this leucine substitution was a pathogenic mutation causing gss in these families. Another mutation had previously been reported in the PrP gene consisting of 144 base pair (b.p.) insertion in a U.K. family with Creutzfeldt-Jakob disease (Owen et al. 1989). Since the report of these first two mutations a large number of other point mutations and other insertional mutations have now been reported in the PrP gene in affected or at risk individuals in families with these inherited diseases. Formal demonstration that the leucine 102 mutation was pathogenic was provided by Hsiao et al. (1990), who demonstrated that transgenic mice encoding multiple copies of a prion protein transgene encoding leucine at the corresponding murine codon spontaneously developed spongiform neurodegeneration. It has further been demonstrated that brain homogenates from such spontaneously sick transgenic mice can transmit the disease to wild-type animals (Hsiao et al. 1992). This production of a transmissible disease by mutation of a single amino acid in the prion protein argues strongly in favour of the prion protein, or rather an abnormal isoform of this protein, being the principal constituent of the transmissible agent or prion.

The availability of direct gene markers for the inherited diseases has enabled study of the phenotypic range of these disorders. Using DNA markers it has been possible to demonstrate remarkable phenotypic heterogeneity within families and also to identify some previously unrecognized prion diseases. Initial observations in this regard were made in the kindred with the 144 b.p. insertion in the PrP gene (Owen et al.

1989). The diagnosis of familial cpp in this kindred was based on an individual who died in the 1940s with both a clinical and neuropathological diagnosis of CID. Indeed, the typicality of the histopathological features of this case have led to its inclusion illustrating CID pathology in Greenfield's Neuropathology Textbook. The clinical course was said to be characteristic of CID with a six-month duration. However another affected individual from this family had a duration of illness of over four years and at autopsy only mild and subtle spongiform changes, insufficient for a morphological diagnosis of CID, were seen in the hippocampus. An additional family member has had the illness for over 12 years. Therefore a range of illness from that of classical sub-acute cjp to a GSS-like picture exceeding the longest previously published clinical duration for gss can co-exist in the same family with the same genetic mutation. Additionally the histological features can vary from gross to minimal. For this reason it was argued that other GSS/CJD-type illnesses might present atypically and mimic other neurodegenerative conditions. This led to screening of neurodegenerative cases and the identification of families with mutations in the PrP gene who were not thought on clinical ground to be suffering from spongiform encephalopathies. The first family to be detected in this way using PrP gene analysis had been thought clinically to be suffering from familial Alzheimer's disease (Collinge et al. 1989). Further screening of over 100 cases revealed a further four families with an identical PrP gene insertion (Owen et al. 1991) and subsequent genealogical investigation demonstrated that all these cases form part of a single large kindred in the southeast of England (Poulter et al. 1992). Previous clinical diagnosis in these families had included familial Alzheimer's disease, Huntington's disease, Pick's disease and familial presenile dementia (Collinge et al. 1992). Of particular interest in this regard was a family which had carried previous clinical diagnoses of Huntington's disease and familial Alzheimer's disease. The clinical features of one member of this family were most unusual. The patient had a long-standing personality disorder characterized by irritability, aggression, antisocial behaviour and hypersexuality. He became increasingly aggressive in his early 20s and developed loss of balance and dysarthria. By his late 20s he had developed obvious intellectual decline, memory loss and a profound dyspraxia. At age 30 he had negligible abilities on verbal tasks, severe memory impairment, gross ataxia and episodes of clonic activity later developing generalized seizures. By age 36 he was permanently hypertonic, unable to talk and died of bronchial pneumonia. At autopsy there was mild cerebral atrophy but a remarkable absence of histological features of cJD, GSS or Alzheimer's disease. This finding raised the possibility that prion diseases were under-diagnosed, as perhaps 10% of patients dying with dementia who undergo autopsy do not have sufficient histological findings to reach a diagnosis (Collinge et al. 1990). Therefore diagnostic terms such as cJD, GSS and spongiform encephalopathy are becoming less useful with the demonstration that CJD and GSS form part of a wider spectrum of disease and can coexist in the same family with the same mutation. The histological features regarded as being characteristic of these disorders are not invariably present. Since an aberrant form of the prion protein and its gene play a key role in the aetiology of these conditions, prion disease, which can then be subdivided into acquired, sporadic and inherited forms, seems a more suitable terminology.

2. INHERITED PRION DISEASES

At least 18 pathogenic mutations are now recognized within the PrP gene leading to the inherited prion diseases. The identification of one of these mutations allows molecular diagnosis in an affected case. In addition such work has led to further insights into the phenotypic range of these disorders which now extends well beyond that previously realized. Pathogenic mutations reported to date in the human PrP gene are of two groups: (i) point mutations within coding sequence resulting in amino-acid substitutions (or in one case, in a stop codon, with production of a truncated protein) in PrP at residues 102, 105, 117, 145, 178, 180, 198, 200, 210, 217 and 232; and (ii) insertional mutations encoding 2, 4, 5, 6, 7, 8 or 9 additional copies of an octapeptide repeat that is present in a tandem array of five copies in the normal protein.

While cases within the 144 b.p. insertion pedigree clinically resembled Alzheimer's disease a number of types of inherited prion disease have now been identified that not only clinically but also in many respects histologically resemble Alzheimer's disease. Inherited prion disease (PrP 216 b.p. insertion) shows no spongiform encephalopathy histologically, but marked plague deposition (Duchen et al. 1993). In the hippocampus there are neuritic plaques positive for both β-amyloid protein and tau. In the cerebellum and basal ganglia the plaques are PrP positive. Neurofibrillary tangles were also seen. Recently reported is a point mutation resulting in an amber mutant at codon 145 (Kitamoto et al. 1993). This case phenotypically appeared like Alzheimer's disease, both at the clinical and neuropathological level. The plaques were however PrP positive. In the case of inherited prion disease (PrP serine 198) and inherited prion disease (PrP arginine 217) as well as prominent PrP-positive plaques there are large numbers of neurofibrillary tangles which are antigenically and morphologically indistinguishable from those seen in Alzheimer's disease (Hsiao et al. 1992).

Since the first report of a six octarepeat insertional mutation in PrP a whole family of insertional mutations are now recognized (Goldfarb et al. 1991a; Owen et al. 1992). Insertions have not been described in normal individuals (other than individuals at risk in affected families) with the exception of a four octarepeat insertion reported in an individual who died at age 63 of hepatic cirrhosis (Goldfarb et al. 1991a). Recently, we have identified a patient with a classical phenotype of cjp (both clinically and histologically) with a four octarepeat insertion. Although this mutation differs from that published by Goldfarb et al.

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at the nucleotide level, the same protein is encoded (J. Collinge & M. S. Palmer, unpublished results). This may represent incomplete penetrance of this mutation.

Of particular interest has been the finding of a mutation at codon 178 in several families with what is described as fatal familial insomnia (Medori et al. 1992a,b). This disease is characterized by progressive untreatable insomnia and autonomic dysfunction. This disease has now been reclassified as one of the inherited prion diseases and, interestingly, carries the same mutation as that seen in several families from Northern Europe with a phenotype like Creutzfeldt–Jakob disease (Goldfarb et al. 1991b).

Although cJD usually occurs as a sporadic disease without clustering of cases, there are three well-documented ethnogeographic clusters of cJD that were an apparent exception to this random distribution of cases, amongst Libyan Jews, in an area of Slovakia and in Chile. All three clusters are now known to be familial and associated with the codon 200 mutation (Goldfarb et al. 1990a,b; Hsiao et al. 1991; Brown et al. 1992a). Cases of inherited prion disease (PrP lysine 200) have now been identified in the U.K., and at least one of these has no apparent genealogical link to the known clusters suggesting a separate U.K. focus of this disease (Collinge et al. 1993).

The availability of such direct gene tests for the inherited forms of these diseases allows not only unequivocal diagnosis but also presymptomatic testing of unaffected but at risk family members (Collinge et al. 1991b) and also opens up the potential for antenatal testing. In some families it may also be possible to determine whether a gene carrier will have an early or late onset of disease by codon 129 genotyping (discussed later). Most of the inherited prion diseases described to date show full penetrance although information is still very limited on a large number of these mutations. A particular exception is inherited prion disease (PrP leucine 200) in which elderly unaffected gene carriers have been identified. The genetic counselling situation in many respects resembles that seen in Huntington's disease and it is important to appreciate that performing PrP gene analysis for diagnostic purposes may have important consequences for other family members and that such issues should be discussed with the family prior to

In addition to pathogenic PrP mutations, a number of coding and non-coding polymorphisms have been described. A common protein polymorphism at residue 129 is known to be important in genetic susceptibility to prion diseases (see below). Deletions of a single octarepeat element have been reported both in patients and normal controls (Laplanche *et al.* 1990; Diedrich *et al.* 1992). We studied 482 patients with a range of neurodegenerative illnesses including acquired, sporadic and inherited prion diseases and 255 unrelated caucasian normal controls and found five deletions in the patient group (0.52% of alleles) and two deletions in the controls (0.39% of alleles). However, only one of the deletions was in a definite CID case. This difference in frequency was not statis-

tically significant and we estimated a population frequency of deletions in caucasians as 1% of the population. We identified three different deletions at the nucleotide level although all encode the same protein (Palmer *et al.* 1993). There is no evidence therefore that deletions are associated with disease. It remains to be established if their co-occurence in a family with an inherited prion disease may produce a modification of the phenotype.

3. IATROGENIC PRION DISEASE

Although prion diseases can be transmitted to experimental animals by intracerebral inoculation with brain homogenates, it is important to appreciate that they are not contagious conditions in humans. Documented case-to-case spread in humans has only occurred as a result of ritualistic cannibalism in the case of kuru or in Western societies as a result of accidental inoculation with prions. Such iatrogenic routes include the use of inadequately sterilized intracerebral electrodes, dura mater and corneal grafting, and from the use of human cadaveric pituitaryderived growth hormone or gonadotrophin. These cases are extremely rare. It is of interest that cases arising from intracerebral or optic inoculation manifest clinically with a phenotype reminiscent of classical Creutzfeldt-Jakob disease with a rapidly progressive dementia, while those resulting from a peripheral route of inoculation with the agent present usually as a progressive cerebellar syndrome, reminiscent of kuru.

We investigated the possibility that genetic susceptibility may have a part to play in the occurrence of iatrogenic cjd. We chose to look at a group of individuals who had unfortunately developed CJD following treatment with human pituitary derived growth hormone. At the time of study six cases had arisen in the U.K., 1908 individuals having been treated with hormone derived from human pituitary. In addition a single case had arisen in the U.K. as a result of treatment with pituitary derived gonadotrophin in Australia. It was known that no single batch of hormone spanned all the cases and that such batches were prepared from pools of very large numbers of glands (up to 3000). It therefore seemed possible, if not likely, that most of the patients treated with growth hormone were exposed to the same amount of the transmissible agent. We hypothesized therefore that the ones that went on to get CJD may represent a genetically susceptible population. Known pathogenic mutations were excluded from all cases but the distribution of genotypes with respect to a common polymorphism in the PrP was quite different from the population frequencies. There is a common polymorphism in human PrP at residue 129, methionine being encoded in 63% of alleles and valine in 37% of alleles in Caucasians. This gives a genotype frequency of 37% Met/Met 21% Met/Val and 12%Val/Val (as estimated using a sample population of 106 normal controls). However, of the seven iatrogenic cjp samples analyzed, four were Val/Val, two were Met/Val and only one Met/Met (Collinge et al.

1991a). Although the number of cases analysed was necessarily small (but included all U.K. pituitary hormone related iatrogenic CID at the time of the study) the data suggested that there was genetic susceptibility to exogenous prion infection. Individuals exposed to contaminated pituitary hormones who are valine homozygotes may be at increased risk (albeit still a small risk) of developing cjp. Similar results have now been reported in U.S. pituitary hormone cases (Brown et al. 1992b). The implications of this data with respect to a general model of prion propagation are discussed later. It is possible that iatrogenic сдо cases arising from intracerebral or optic inoculation with prions may not show such an effect as the intracerebral route of inoculation is known to be very much more efficient than a peripheral route. We have genotyped only one such case, related to dura mater grafting, and the genotype was Met/Met. It will be of interest to see if cases of kuru occur predominantly in a Val homozygous genotype.

4. SPORADIC PRION DISEASE

Most cases of human prion disease currently recognized occur as sporadic cjp. By definition there will not be a family history in such cases. However, we have on occasion found pathogenic mutations in apparently sporadic cases. With a late onset disease, family history may not be immediately apparent. The parent with the mutation may of course have died from another illness prior to the development of neurodegeneration. Additionally, non-paternity accounts for a number of such cases. With these exceptions however most sporadic cpp is of unknown aetiology. Our finding of the importance of genotype at codon 129 in genetic susceptibility to iatrogenic prion disease led us to genotype a sample of sporadic CJD cases. If sporadic CJD were being acquired from some environmental source of prions, for instance from scrapie infected sheep or another animal source there may also be an over representation of the valine 129 homozygous genotype. We initially studied 22 wellcharacterized sporadic cyp cases and found that all but a single case were homozygous either to methionine or valine at codon 129 (Palmer et al. 1991). There was no significant excess of valine homozygotes. Although 51% of the normal caucasian population are heterozygotes, nearly all sporadic CID appears to occur in homozygotes. This finding has now been replicated on a larger series in conjunction with the U.K. CJD Surveillance Unit (J. Collinge, M. S. Palmer and R. G. Will, unpublished). The implications of this finding will be discussed below.

5. A MODEL OF PRION PROPAGATION

In 1990 Prusiner and colleagues demonstrated that the species barrier to transmission of prion disease from hamsters to mice could be overcome by overexpression of normal hamster prion protein in transgenic mice (Prusiner *et al.* 1990). Although prion

diseases can be transmitted between mammalian species by inoculation, in practice it is difficult to do so, and typically transmission occurs in only a small proportion of inoculated animals and then only after prolonged incubation periods. When such transgenic mice were challenged with mouse derived prions, the infectivity they produced was fully pathogenic for mice but not hamsters, whereas on challenge with hamster derived prions they produced prions fully pathogenic to hamsters but not mice. This finding has been interpreted as implying that a direct interaction between PrP molecules occurs at some stage in the process of prion propagation and that the efficiency of such interaction is dependent on the degree of sequence homology between the interacting species. As there are a number of amino acid differences between murine and hamster PrP interaction between the two forms would be less favoured than interaction between PrP molecules with the same primary structure. Such work has led to the idea that replication of prions may occur by the abnormal isoform of PrP, PrPSc, interacting directly, either by dimerization or more complex interaction, with the normal cellular isoform, PrPC, and catalysing the conversion of PrPC to PrPSc (Prusiner et al. 1990; Weissmann 1991). Such an effect could then lead to a chain reaction of conversion leading to the progressive accumulation of the abnormal, and partly protease resistant isoform. This could then produce disease either by progressive loss of PrP function or alternatively by cellular damage resulting from accumulation of the protease resistant isoform. Clearly, the implication is that the pathogenic mutations in the prion protein result in the production of a protein that may convert spentaneously to PrPSc in individuals with inherited prion diseases. Once produced, PrPSc will then produce the same catalytic chain reaction as hypothesized in cases where PrPSc is inoculated. Such a model provides an explanation of how a disease can be simultaneously inherited and transmissible. The finding that nearly all sporadic cpp occurs in homozygotes with respect to a common and apparently innocent protein polymorphism lends strong support to such a mechanism (Palmer et al. 1991). Again prion protein interaction would occur most favourably in individuals with two identical copies of the prion protein. Heterozygotes producing two different proteins would be somewhat protected, as if by an internal 'species barrier'. It is possible that the occasional individuals heterozygous at codon 129 who do develop sporadic CID have a more prolonged illness although more detailed studies are required to investigate this further (Collinge et al. 1991). Further evidence for this model of prion replication is provided by the observation that in inherited prion disease (PrP 144 b.p. insertion) the age at onset of the disease is 1-2 decades later in individuals heterozygous at codon 129 than homozygotes at codon 129 (Baker et al. 1991). This effect has now been observed in additional inherited prion disease kindreds.

We argued that PrP valine 129 and PrP methionine 129 will differ slightly in their propensity to convert to PrP^{Sc}. The excess of PrP valine 129 homozygotes

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amongst human pituitary hormone related cases suggests that PrP valine 129 may be the more susceptible (Collinge et al. 1991a). Valine homozygotes would therefore be the most susceptible to prion diseases following environmental exposure to prions while heterozygotes would be partially protected. However, the genotype of the inoculum clearly will be relevant and it can not be assumed that val 129 homozygotes would also have increased susceptibility to animal prions compared to met 129 homozygotes. However, heterozygotes should still be protected according to such a model. Such ideas are supported by the recent finding (Büeler et al. 1993) that mice heterozygous for an ablated PrP allele, and which have approximately 50% of normal PrP expression, are highly resistant to prion disease following experimental inoculation, having extremely prolonged incubation times and also prolonged durations of illness.

6. CONCLUSIONS

The human prion diseases can be subdivided into inherited, sporadic and acquired forms. All currently recognized inherited prion diseases are caused by coding mutations in the PrP gene. It is not yet clear whether all of these 18 types of inherited prion disease will prove to be transmissible to experimental animals. It is possible that some of them may only be transmissible to transgenic animals expressing an homologous PrP. Some may have a different disease mechanism not producing infective prions but rather represent prion protein diseases. Sporadic prion disease occurs mainly in homozygotes with respect to a common PrP polymorphism. These cases could conceivably arise by somatic mutation producing one of the pathogenic PrP mutations, resulting in production of prions in the cell (or clone of cells) with the mutation, then leading to a progressive disease. Alternatively spontaneous conversion of PrP^{C} to PrP^{Sc} may occur as a rare stochastic event in the wild-type protein. Recent work indicating that transgenic mice with extremely high levels of hamster PrPC production spontaneously develop a prion disease raises the additional possibility that some cases of inherited or sporadic prion disease may be caused by overexpression of PrP^C, either resulting from polymorphism in the PrP gene regulatory elements, the involvement of other genes, or environmental factors. Acquired prion diseases are caused direct inoculation with prions either by ritualistic cannibalism or iatrogenic routes. At least in the case of pituitary hormone related cases where low dose, peripheral inoculation resulted in the illness, genetic susceptibility is an important factor. It remains to be seen if the dietary exposure to bovine prions will result in transmission to humans. Recent success in removing the species barrier between hamsters and mice in transgenic mice raises the possibility that it may be possible to generate transgenic mice expressing human PrP variants that will be highly susceptible to human prion diseases, and in which the effectiveness of the bovine-human species barrier can be experimentally addressed.

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